#11
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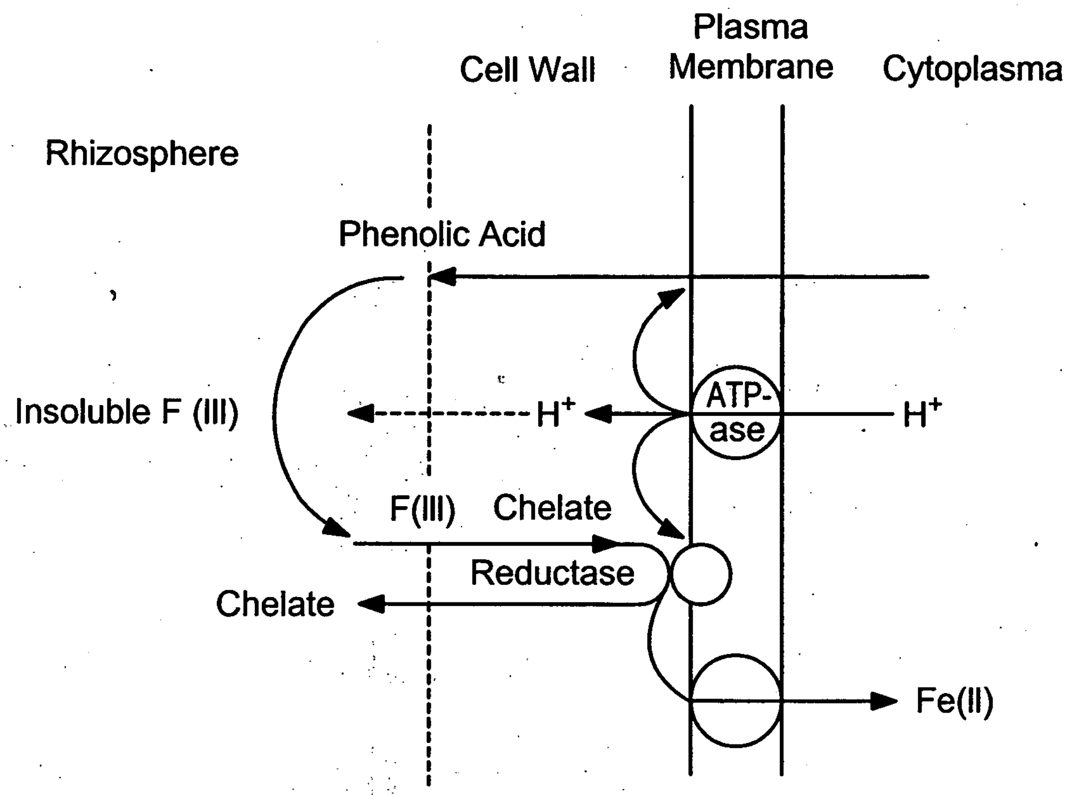
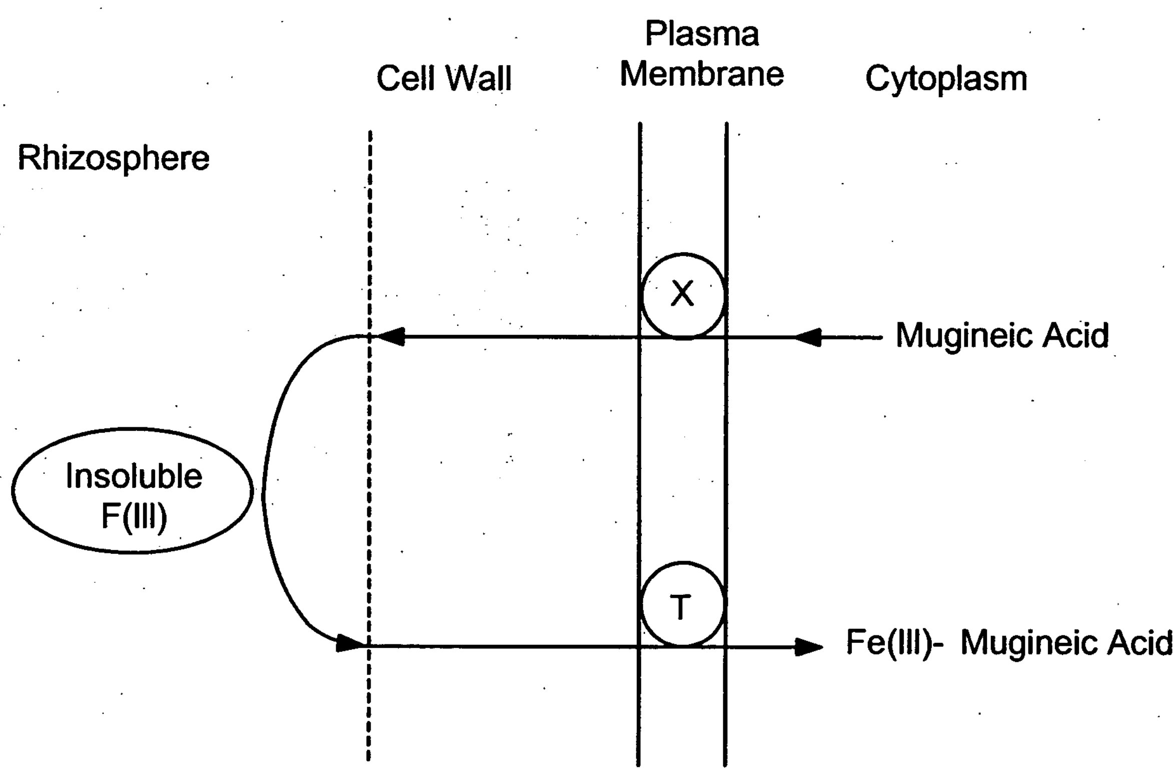


FIG. 1



Two Kinds of Fe-Uptake Mechanisms in Higher Plants

FIG. 2

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Seq 37

```
      putative           poly(A)                          putative          poly (A)
    poly(A) signal         site                         poly(A) signal        site
541 TCCGTCAAAAAATCACTTATTTATCCTTCTGTTTACAAAGATTATAATGAACGAACTTTTTATTTATGGAAGCGTCTACCATTTAATTTT 630
181  S  V  K  K  S  L  I  Y  P  S  V  Y  K  D  Y  N  E  R  T  F  Y  L  W  K  R  L  P  F  N  F  210

                    putative        poly(A)  poly(A)
                 poly(A) signal      site     site
631 ACAACTCGAGGCAAGGGTCTCGTCGTATTAATTTTTGTTATTTTGACTATATTATCTCTCAGTTTTGGTCATAATATTAAACTTCCACAC 720
211  T  T  R  G  K  G  L  V  V  L  I  F  V  I  L  T  I  L  S  L  S  F  G  H  N  I  K  L  P  H  240
```

FIG. 3

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1	ATGGTTAGAACCCGTGTATTATTCTGGTTATTTATATCTTTTTTTGCTACGGTTCAATCG	60
61	AGTGCTAGACTTATTAGCACTTCATGTATTTCCCAAGCTGCGCTATACCAATTTGGATGT	120
121	TCTAGTAAATCTAAAAGTTGCTACTGTAAAAACATCAATTGGCTGGGTTCAGTGACAGCA	180
181	TGTGCCTATGAGAATTCCAAATCTAACAAAACACTAGACAGCGCCTTAATGAAGTTAGCA	240
241	TCCCAATGTTCAAGCATCAAAGTTTATACTTTAGAGGACATGAAGAATATTTATTTAAAT	300
301	GCGTCAAATTATTTGAGAGCACCTGAGAAAAGTGATAAAAAAACCGTGGTTAGTCAACCG	360
361	CTCATGGCGAACGAGACAGCGTATCATTATTATTATGAGGAAAATTATGGTATCCATCTT	420
421	AACCTAATGCGCTCTCAATGGTGGGGTTGGGGTGTGGTGTTCTTGTGGGTGGGTGTGGTT	480
481	ACTGCAGCCACTATCTTGAACATTCTGAAAAGGGTGTTTGGTAAGAACATCATGGCAAAC	540
541	TCCGTCAAAAAATCACTTATTTATCCTTCTGTTTACAAAGATTATAATGAACGAACTTTT	600
601	TATTTATGGAAGCGTCTACCATTTAATTTTACAACTCGAGGCAAGGGTCTCGTCGTATTA	660
661	ATTTTTGTTATTTTGACTATATTATCTCTCAGTTTTGGTCATAATATTAAACTTCCACAC	720
721	CCATATGATAGGCCCAGATGGAGAAGAAGTATGGCCTTTGTGAGTCGTAGAGCAGACTTG	780
781	ATGGCCATTGCACTTTTCCCAGTAGTCTATCTATTCGGAATAAGAAATAATCCCTTCATC	840
841	CCTATAACAGGGCTTTCCTTTTCTACATTTAATTTCTATCATAAATGGTCTGCCTACGTT	900
901	TGTTTCATGTTGGCCGTTGTACACTCAATTGTCATGACCGCCTCGGGAGTGAAAAGAGGT	960
961	GTGTTTCAAAGTCTGGTTAGGAAATTTTACTTTAGGTGGGGTATAGTGGCAACGATATTA	1020
1021	ATGTCTATTATTATTTTCCAAAGTGAAAAAGTATTTAGAAATAGAGGGTATGAGATATTC	1080
1081	CTTCTTATTCATAAAGCGATGAATATTATGTTCATTATTGCCATGTACTACCATTGTCAC	1140
1141	ACCCTGGGCTGGATGGGTTGGATTTGGTCAATGGCTGGTATTTTATGCTTTGATAGATTC	1200
1201	TGCAGGATTGTTAGAATAATCATGAATGGTGGCTTGAAAACTGCTACTTTGAGTACCACT	1260
1261	GATGATTCTAATGTTATTAAAATTTCAGTAAAAAAACCAAAGTTTTTCAAGTACCAAGTA	1320
1321	GGAGCTTTCGCATACATGTATTTCTTATCACCAAAAAGTGCATGGTTCTATAGTTTCCAA	1380
1381	TCACATCCATTTACAGTATTATCGGAACGACACCGTGATCCAAACAATCCAGATCAATTG	1440
1441	ACGATGTACGTAAAGGCAAATAAAGGTATCACTCGAGTTTTGTTATCGAAAGTTCTAAGT	1500
1501	GCTCCAAATCATACTGTTGATTGTAAAATATTCCTTGAAGGCCCATATGGTGTAACGGTT	1560
1561	CCACATATCGCTAAGCTAAAAAGAAATCTGGTAGGTGTAGCCGCTGGTTTGGGTGTTGCG	1620
1621	GCTATTTATCCGCACTTTGTCGAATGTTTACGGTTACCATCTACTGATCAACTTCAGCAT	1620
1681	AAATTTTACTGGATTGTTAATGACCTATCCCATTTGAAATGGTTTGAAAATGAATTGCAA	1740
1741	TGGTTAAAGGAGAAAAGTTGTGAAGTCTCAGTCATATATACTGGTTCCAGTGTTGAGGAC	1800
1801	ACAAATTCAGATGAGAGTACAAAAGGTTTTGATGATAAAGAAGAAAGCGAAATCACTGTT	1860
1861	GAATGTCTCAATAAAAGACCTGATTTGAAAGAACTAGTGCGCTCGGAAATAAAACTCTCA	1920
1921	GAACTAGAGAATAATAATATTACCTTTTATTCCTGCGGGCCAGCAACGTTTAACGACGAT	1980
1981	TTTAGAAATGCAGTGGTCCAAGGTATAGACTCTTCCTTGAAGATTGACGTTGAACTAGAA	2040
2041	GAAGAAAGTTTTACATGGT	2059

FIG. 4

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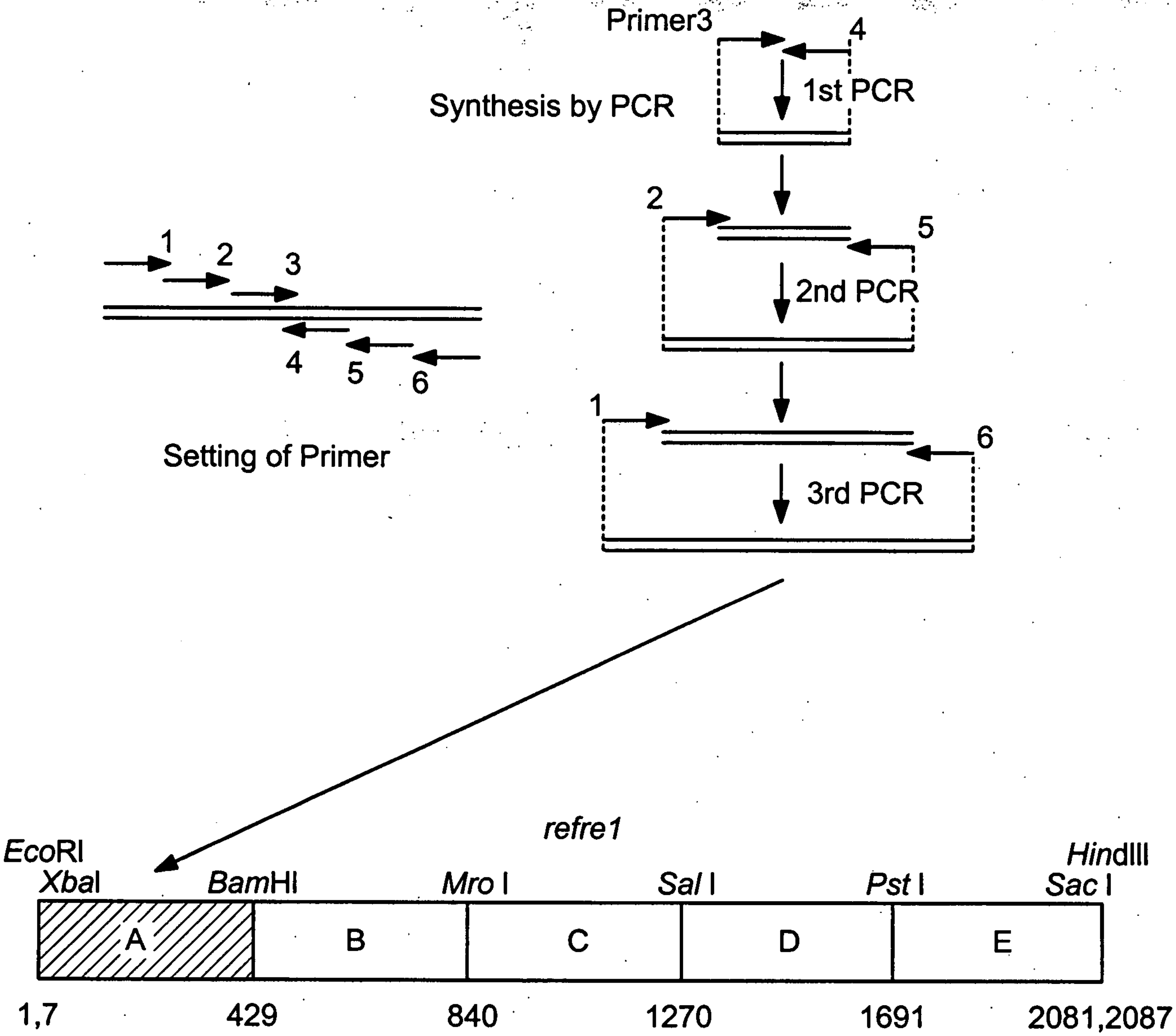

FIG. 5

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FIG. 6A
FIG. 6B

FIG. 6

Sequence Name	Base Sequence 5' … 3'	
A-1	GAATTCTCTAGACTCCACCATGGTTAGAACCAGAGTCCTTTTCTGCCTCTTCATCTCTTTCTTCGCTACAGTCCAATCGAGCG	83mer
A-2	GTCCAATCGAGCGCTACACTCATCTCCACTTCATGCATTTCTCAGGCTGCACTGTACCAGTTCGGATGCTCAAGCAAGTCAAA	83mer
A-3	CAAGCAAGTCAAAGTCTTGCTACTGCAAGAACATCAATTGGCTCGGAAGCGTCACTGCATGCGCTTATGAGAACTCCAAATCT	83mer
A-4	TCCAGTGTGTAAACCTTGATACTTGAGCATTGGCTGGCAAGTTTCATCAAAGCGGAGTCCAGAGTCTTGTTAGATTTGGAGTT	83mer
A-5	TGTCTTCTTATCGGATTTCTCAGGAGCGCGAAGGTAGTTACTTGCATTAAGGTAGATGTTCTTCATGTCCTCCAGTGTGTAAA	83mer
A-6	GGATCCCATAGTTTTCCTCATAGTAGTAGTGATAGGCCGTCTCATTTGCCATCAACGGTTGTGAAACAACTGTCTTCTTATCG	83mer
B-1	GGATCCACTTGAATTTGATGCGATCTCAATGGTGCGCATGGGGCCTCGTCTTCTTCTGGGTCGCAGTCCTTACCGCCGCA	80mer
B-2	CCTTACCGCCGCAACTATCTTGAACATTCTCAAACGCGTATTCGGCAAGAACATTATGGCAAATTCTGTTAAGAAGTCTC	80mer
B-3	GTTAAGAAGTCTCTTATCTACCCAAGCGTTTACAAAGACTACAACGAGAGAACTTTCTATCTTTGGAAACGTTTGCCATT	80mer
B-4	AGAGTGAGAGAATAGTCAGAATGACAAAGATAAGAACTACGAGTCCTTTGCCTCGAGTTGTAAAGTTGAATGGCAAACGT	80mer
B-5	AATGCCATTGATCTTCTCCATCTAGGTCTATCGTAAGGATGTGGCAACTTGATGTTATGTCCGAAAGAGAGTGAGAGAAT	80mer
B-6	TCCGGATACCGAAAAGGTACACCACGGGGAAAAGAGCGATTGCCATCAAGTCAGCACGGCGTGAGACGAATGCCATTGAT	80mer
C-1	TCCGGAACAACCCCTTCATCCCAATCACCGGATTGAGCTTTAGTACTTTCAACTTTTACCACAAATGGTCAGCATACGTCTGC	83mer
C-2	GCATACGTCTGCTTCATGTTAGCCGTCGTCCATTCAATCGTTATGACCGCTTCAGGAGTTAAACGAGGAGTATTCCAGTCTCT	83mer
C-3	TATTCCAGTCTCTTGTAAGGAAATTCTACTTCAGATGGGGAATAGTAGCCACAATTCTTATGTCCATCATCATTTTCCAGTCC	83mer
C-4	ATAAACATGATGTTCATGGCTTTGTGAATAAGTAAGAAGATTTCATAACCTCGGTTCCTGAAGACCTTCTCGGACTGGAAAAT	83mer
C-5	GAGGATGCCAGCCATGGACCAGATCCAGCCCATCCATCCTAGTGTGTGGCAATGGTAATACATAGCTATGATAAACATGATGT	83mer
C-6	GTCGACAAAGTGGCGGTCTTAAGACCTCCGTTCATGATGATACGTACAATTCGGCAGAACCTGTCGAAGCAGAGGATGCCAGC	83mer

FIG. 6A

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D-1	GTCGACCACAGATGATTCTAACGTTATCAAGATCTCTGTCAAGAAGCCTAAGTTCTTCAAGTATCAAGTGGGAGCATTTGCC	82mer
D-2	GGAGCATTTGCCTATATGTACTTTCTTTCACCAAAATCAGCCTGGTTCTACAGTTTTCAATCTCATCCCTTCACAGTCCTAT	82mer
D-3	TTCACAGTCCTATCAGAAAGGCACAGAGATCCTAACAACCCAGATCAACTAACTATGTACGTCAAAGCTAACAAGGGCATTA	82mer
D-4	CCTCTAAGAAAATCTTGCAATCAACGGTATGGTTTGGAGCGCTTAGAACTTTGCTAAGAAGTACTCTCGTAATGCCCTTGTT	82mer
D-5	GGCCCGCAGCTACTCCTACTAGATTTGTCTTAAGTTTGGCAATGTGAGGGACAGTTACGCCATATGGTCCCTCTAAGAAAAT	82mer
D-6	CTGCAGTTGATCAGTGCTAGGCAATCTAAGGCATTCTACGAAATGGGGGTAGATGGCTGCCACGCCGAGGCCCGCAGCTACT	82mer

E-1	CTGCAGCACAAGTTCTACTGGATCGTCAACGACCTTAGTCACCTTAAGTGGTTCGAAAACGAGCTACAATGGCTTAA	77mer
E-2	ACAATGGCTTAAGGAGAAATCTTGTGAAGTCTCTGTCATCTACACTGGGTCATCAGTGGAGGATACAAACTCAGATG	77mer
E-3	CAAACTCAGATGAGTCCACTAAGGGTTTCGATGACAAGGAAGAATCTGAAATCACCGTAGAATGCCTTAACAAGAGG	77mer
E-4	GTGATGTTGTTGTTCTCGAGTTCTGACAATTTGATCTCTGATCTCACTAGCTCTTTGAGGTCTGGCCTCTTGTTAAG	77mer
E-5	CGATACCTTGTACAACTGCATTCCTAAAGTCGTCATTGAAAGTCGCTGGTCCGCATGAGTAGAAAGTGATGTTGTTG	77mer
E-6	AAGCTTGAGCTCTTACCAAGTAAAACTCTCCTCCTCTAGTTCGACATCTATCTTCAGACTAGAATCGATACCTTGTA	77mer

FIG. 6B

FIG. 7A
FIG. 7B
FIG. 7C

FIG. 7

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```
                                                                                                  A-1
  1 GAATTCTCTAGACTCCACCATGGTTAGAACCAGAGTCCTTTTCTGCCTCTTCATCTCTTTCTTCGCTACAGTCCAATCGAGCGCTACACTCATCTCCACTTCATGCATTTCTCAGGCTGC 120
  1 CTTAAGAGATCTGAGGTGGTACCAATCTTGGTCTCAGGAAAAGACGGAGAAGTAGAGAAAGAAGCGATGTCAGGTTAGCTCGCGATGTGAGTAGAGGTGAAGTACGTAAAGAGTCCGACG 120
    EcoIII  XbaI

                             A-2                                                                          A-3
121 ACTGTACCAGTTCGGATGCTCAAGCAAGTCAAAGTCTTGCTACTGCAAGAACATCAATTGGCTCGGAAGCGTCACTGCATGCGCTTATGAGAACTCCAAATCTAACAACACTCTGGACTC 240
121 TGACATGGTCAAGCCTACGAGTTCGTTCAGTTTCAGAACGATGACGTTCTTGTAGTTAACCGAGCCTTCGCAGTGACGTACGCGAATACTCTTCAGGTTTAGATTGTTCTGAGACCTGAG 240
                                                                                                              A-4

241 CGCTTTGATGAAACTTGCCAGCCAATGCTCAAGTATCAAGGTTTACACACTGGAGGACATGAAGAACATCTACCTTAATGCAAGTAACTACCTTCGCGCTCCTGAGAAATCCGATAAGAA 360
241 GCGAAACTACTTTGAACGGTCGGTTACGAGTTCATAGTTCCAAATGTGTGACCTCCTGTACTTCTTGTAGATGGAATTACGTTCATTGATGGAAGCGCGAGGACTCTTTAGGCTATTCTT 360
                                                  A-5                                                                 A-6

361 GACAGTTGTTTCACAACCGTTGATGGCAAATGAGACGGCCTATCACTACTACTATGAGGAAAACTATGGGATCCACTTGAATTTGATGCGATCTCAATGGTGCGCATGGGGCCTCGTCTT 480
361 CTGTCAACAAAGTGTTGGCAACTACCGTTTACTCTGCCGGATAGTGATGATGATACTCCTTTTGATACCCTAGGTGAACTTAAACTACGCTAGAGTTACCACGCGTACCCCGGAGCAGAA 480
                                B-1                                          BamHI
                                                                                                 B-2
481 CTTCTGGGTCGCAGTCCTTACCGCCGCAACTATCTTGAACATTCTCAAACGCGTATTCGGCAAGAACATTATGGCAAATTCTGTTAAGAAGTCTCTTATCTACCCAAGCGTTTACAAAGA 600
481 GAAGACCCAGCGTCAGGAATGGCGGCGTTGATAGAACTTGTAAGAGTTTGCGCATAAGCCGTTCTTGTAATACCGTTTAAGACAATTCTTCAGAGAATAGATGGGTTCGCAAATGTTTCT 600

                                             B-3
601 CTACAACGAGAGAACTTTCTATCTTTGGAAACGTTTGCCATTCAACTTTACAACTCGAGGCAAAGGACTCGTAGTTCTTATCTTTGTCATTCTCACTATTCTCTCACTCTCTTTCGGACA 720
601 GATGTTGCTCTCTTGAAAGATAGAAACCTTTGGAAACGGTAAGTTGAAATGTTGAGCTCCGTTTCCTGAGCATCAAGAATAGAAACAGTAAGACTGATAAGAGAGTGAGAGAAAGCCTGT 720
                                         B-4                                                                        B-5
```

FIG. 7A

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```
721 TAACATCAAGTTGCCACATCCTTACGATAGACCTAGATGGAGAAGATCAATGGCATTCGTCTCACGCCGTGCTGACTTGATGGCAATCGCTCTTTTCCCCGTGGTGTACCTTTTCGGTAT 840
721 ATTGTAGTTCAACGGTGTAGGAATGCTATCTGGATCTACCTCTTCTAGTTACCGTAAGCAGAGTGCGGCACGACTGAACTACCGTTAGCGAGAAAAGGGGCACCACATGGAAAAGCCATA 840
```

C-1

B-6

```
841 CCGGAACAACCCCTTCATCCCAATCACCGGATTGAGCTTTAGTACTTTCAACTTTTACCACAAATGGTCAGCATACGTCTGCTTCATGTTAGCCGTCGTCCATTCAATCGTTATGACCGC 960
841 GGCCTTGTTGGGGAAGTAGGGTTAGTGGCCTAACTCGAAATCATGAAAGTTGAAAATGGTGTTTACCAGTCGTATGCAGACGAAGTACAATCGGCAGCAGGTAAGTTAGCAATACTGGCG 960
```

*Mro*I

C-2

C-3

```
961 TTCAGGAGTTAAACGAGGAGTATTCCAGTCTCTTGTAAGGAAATTCTACTTCAGATGGGGAATAGTAGCCACAATTCTTATGTCCATCATCATTTTCCAGTCCGAGAAGGTCTTCAGGAA 1080
961 AAGTCCTCAATTTGCTCCTCATAAGGTCAGAGAACATTCCTTTAAGATGAAGTCTACCCCTTATCATCGGTGTTAAGAATACAGGTAGTAGTAAAAGGTCAGGCTCTTCCAGAAGTCCTT 1080
```

C-4

```
1081 CCGAGGTTATGAAATCTTCTTACTTATTCACAAAGCCATGAACATCATGTTTATCATAGCTATGTATTACCATTGCCACACACTAGGATGGATGGGCTGGATCTGGTCCATGGCTGGCAT 1200
1081 GGCTCCAATACTTTAGAAGAATGAATAAGTGTTTCGGTACTTGTAGTACAAATAGTATCGATACATAATGGTAACGGTGTGTGATCCTACCTACCCGACCTAGACCAGGTACCGACCGTA 1200
```

C-5

C-6

```
1201 CCTCTGCTTCGACAGGTTCTGCCGAATTGTACGTATCATCATGAACGGAGGTCTTAAGACCGCCACTTTGTCGACCACAGATGATTCTAACGTTATCAAGATCTCTGTCAAGAAGCCTAA 1320
1201 GGAGACGAAGCTGTCCAAGACGGCTTAACATGCATAGTAGTACTTGCCTCCAGAATTCTGGCGGTGAAACAGCTGGTGTCTACTAAGATTGCAATAGTTCTAGAGACAGTTCTTCGGATT 1320
```

D-1

*Sal*I

D-2

```
1321 GTTCTTCAAGTATCAAGTGGGAGCATTTGCCTATATGTACTTTCTTTCACCAAAATCAGCCTGGTTCTACAGTTTTCAATCTCATCCCTTCACAGTCCTATCAGAAAGGCACAGAGATCC 1440
1321 CAAGAAGTTCATAGTTCACCCTCGTAAACGGATATACATGAAAGAAAGTGGTTTTAGTCGGACCAAGATGTCAAAAGTTAGAGTAGGGAAGTGTCAGGATAGTCTTTCCGTGTCTCTAGG 1440
```

FIG. 7B

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D-3

1441 TAACAACCCAGATCAACTAACTATGTACGTCAAAGCTAACAAGGGCATTACGAGAGTACTTCTTAGCAAAGTTCTAAGCGCTCCAAACCATACCGTTGATTGCAAGATTTTCTTAGAGGG 1560
1441 ATTGTTGGGTCTAGTTGATTGATACATGCAGTTTCGATTCTTCCCGTAATGCTCTCATGAAGAATCGTTTCAAGATTCGCGAGGTTTGGTATGGCAACTAACGTTCTAAAAGAATCTCCC 1560

D-4 D-5

1561 ACCATATGGCGTAACTGTCCCTCACATTGCCAAACTTAAGAGAAATCTAGTAGGAGTAGCTGCGGGCCTCGGCGTGGCAGCCATCTACCCCCATTTCGTAGAATGCCTTAGATTGCCTAG 1680
1561 TGGTATACCGCATTGACAGGGAGTGTAACGGTTTGAATTCTCTTTAGATCATCCTCATCGACGCCCGGAGCCGCACCGTCGGTAGATGGGGGTAAAGCATCTTACGGAATCTAACGGATC 1680

E-1

D-6

1681 CACTGATCAACTGCAGCACAAGTTCTACTGGATCGTCAACGACCTTAGTCACCTTAAGTGGTTCGAAAACGAGCTACAATGGCTTAAGGAGAAATCTTGTGAAGTCTCTGTCATCTACAC 1800
1681 GTGACTAGTTGACGTCGTGTTCAAGATGACCTAGCAGTTGCTGGAATCAGTGGAATTCACCAAGCTTTTGCTCGATGTTACCGAATTCCTCTTTAGAACACTTCAGAGACAGTAGATGTG 1800

*Pst*I

E-2 E-3

1801 TGGGTCATCAGTGGAGGATACAAACTCAGATGAGTCCACTAAGGGTTTCGATGACAAGGAAGAATCTGAAATCACCGTAGAATGCCTTAACAAGAGGCCAGACCTCAAACAGCTAGTGAG 1920
1801 ACCCAGTAGTCACCTCCTATGTTTGAGTCTACTCAGGTGATTCCCAAAGCTACTGTTCCTTCTTAGACTTTAGTGGCATCTTACGGAATTGTTCTCCGGTCTGGAGTTTCTCGATCACTC 1920

E-4

1921 ATCAGAGATCAAATTGTCAGAACTCGAGAACAACAACATCACTTTCTACTCATGCGGACCAGCGACTTTCAATGACGACTTTAGGAATGCAGTTGTACAAGGTATCGATTCTAGTCTGAA 2040
1921 TAGTCTCTAGTTTAACAGTCTTGAGCTCTTGTTGTTGTAGTGAAAGATGAGTACGCCTGGTCGCTGAAAGTTACTGCTGAAATCCTTACGTCAACATGTTCCATAGCTAAGATCAGACTT 2040

E-5 E-6

2041 GATAGATGTCGAACTAGAGGAGGAGAGTTTTACTTGGTAAGAGCTCAAGCTT 2092
2041 CTATCTACAGCTTGATCTCCTCCTCTCAAAATGAACCATTCTCGAGTTCGAA 2092

*Sac*I *Hind*III

FIG. 7C

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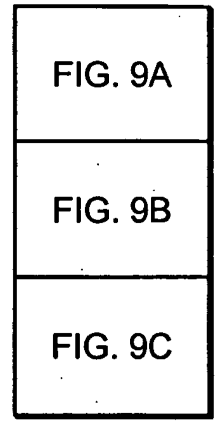

FIG. 9

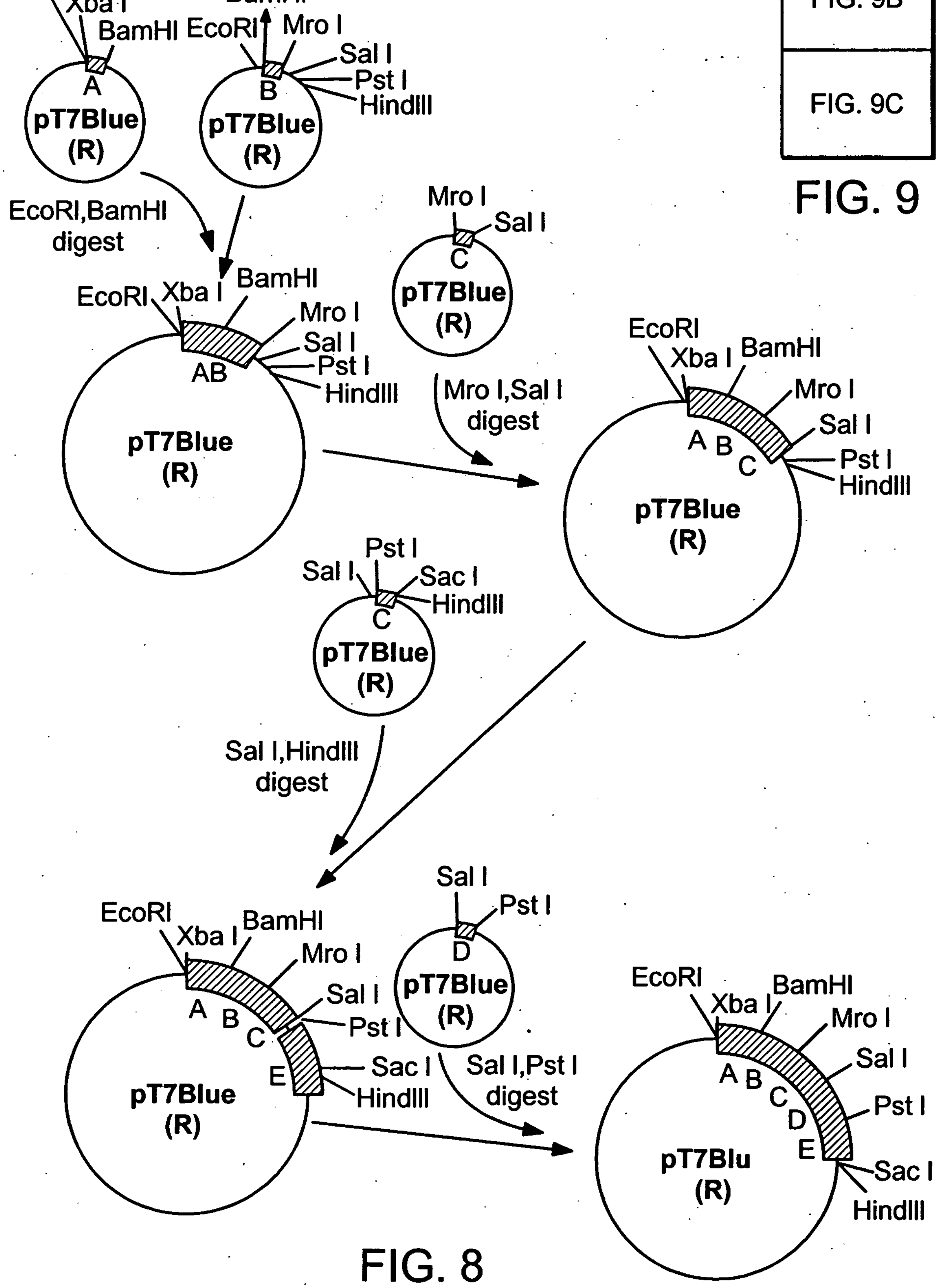

FIG. 8

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```
  1                                                                  gaattctctagactccacc  19

 20 ATGGTTAGAACCAGAGTCCTTTTCTGCCTCTTCATCTCTTTCTTCGCTACAGTCCAATCGAGCGCTACACTCATCTCCACTTCATGCATT 109
  1 M  V  R  T  R  V  L  F  C  L  F  I  S  F  F  A  T  V  Q  S  S  A  T  L  I  S  T  S  C  I   30

110 TCTCAGGCTGCACTGTACCAGTTCGGATGCTCAAGCAAGTCAAAGTCTTGCTACTGCAAGAACATCAATTGGCTCGGAAGCGTCACTGCA 109
 31 S  Q  A  A  L  Y  Q  F  G  C  S  S  K  S  K  S  C  Y  C  K  N  I  N  W  L  G  S  V  T  A   60

200 TGCGCTTATGAGAACTCCAAATCTAACAAGACTCTGGACTCCGGTTTGATGAAACTTGCCAGCCAATGCTCAAGTATCAAGGTTTACACA 289
 61 C  A  Y  E  N  S  K  S  N  K  T  L  D  S  A  L  M  K  L  A  S  Q  C  S  S  I  K  Y  Y  T   90

290 CTGGAGGACATGAAGAACATCTACCTTAATGCAAGTAACTACCTTCGCGCTCCTGAGAAATCCGATAAGAAGACAGTTGTTTCACAACCG 379
 91 L  E  D  M  K  N  I  Y  L  N  A  S  N  Y  L  R  A  P  E  K  S  D  K  K  T  V  V  S  Q  P  120

380 TTGATGGCAAATGAGACGGCCTATCACTACTACTATGAGGAAAACTATGGGATCCACTTGAATTTGATGCGATCTCAATGGTGCGCATGG 469
121 L  M  A  N  E  T  A  Y  H  Y  Y  Y  E  E  N  Y  G  I  H  L  N  L  M  R  S  Q  M  C  A  W  150

470 GGCCTCGTCTTCTTCTGGGTCGCAGTCCTTACCGCCGCAACTATCTTGAACATTCTCAAACGCGTATTCGGCAAGAACATTATGGCAAAT 559
151 G  L  V  F  F  W  V  A  V  L  T  A  A  T  I  L  N  I  L  K  R  V  F  G  K  N  I  M  A  N  180

560 TCTGTTAAGAAGTCTCTTATCTACCCAAGCGTTTACAAAGACTACAACGAGAGAACTTTCTATCTTTGGAAACGTTTGCCATTCAACTTT 649
181 S  V  K  K  S  L  I  Y  P  S  V  Y  K  O  Y  N  E  R  T  F  Y  L  N  K  R  L  P  F  N  F  210
```

FIG. 9A

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```
 650 ACAACTCGAGGCAAAGGACTCGTAGTTCTTATCTTTGTCATTCTGACTATTCTCTCACTCTCTTTCGGACATAACATCAAGTTGCCACAT  739
 211 T  T  R  G  K  G  L  V  V  L  I  F  V  I  L  T  I  L  S  L  S  F  G  H  N  I  K  L  P  H  210

 740 CCTTACGATAGACCTAGATGGAGAAGATCAATGGCATTCGTCTCACGCCGTGCTGACTTGATGGCAATCGCTCTTTTCCCCGTGGTGTAC  829
 241 P  Y  D  R  P  R  W  R  R  S  M  A  F  V  S  R  R  A  D  L  M  A  I  A  L  F  P  V  V  Y  270

 830 CTTTTCGGTATCCGGAACAACCCCTTCATCCCAATCACCGGATTGAGCTTTAGTACTTTCAACTTTTACCACAAATGGTCAGCATACGTC  919
 271 L  F  G  I  R  N  N  P  F  I  P  I  T  G  L  S  F  S  T  F  N  F  Y  H  K  W  S  A  Y  V  300

 920 TGCTTCATGTTAGCCGTCGTCCATTCAATCGTTATGACCGCTTCAGGAGTTAAACGAGGAGTATTCCAGTCTCTTGTAAGGAAATTCTAC 1009
 301 C  F  M  L  A  V  V  H  S  I  V  M  T  A  S  G  V  K  R  G  V  F  G  S  L  V  R  K  F  Y  330

1010 TTCAGATGGGGAATAGTAGCCACAATTCTTATGTCCATCATCATTTTCCAGTCCGAGAAGGTCTTCAGGAACCGAGGTTATGAAATCTTC 1099
 331 F  R  W  G  I  V  A  T  I  L  M  S  I  I  I  F  Q  S  E  K  V  F  R  N  R  G  Y  E  I  F  360

1100 TTACTTATTCACAAAGCCATGAACATCATGTTTATCATAGCTATGTATTACCATTGCCACACACTAGGATGGATGGGCTGGATCTGGTCC 1189
 361 L  L  I  H  K  A  M  N  I  M  F  I  I  A  M  Y  Y  H  C  H  T  L  G  W  M  G  W  I  W  S  390

1190 ATGGCTGGCATCCTCTGCTTCGACAGGTTCTGCCGAATTGTACGTATCATCATGAACGGAGGTCTTAAGACCGCCACTTTGTCGACCACA 1279
 391 M  A  G  I  L  C  F  D  R  F  C  R  I  V  R  I  I  M  N  G  G  L  K  T  A  T  L  S  T  T  420

1280 GATGATTCTAACGTTATCAAGATCTCTGTCAAGAAGCCTAAGTTCTTCAAGTATCAAGTGGGAGCATTTGCCTATATGTACTTTCTTTCA 1369
 421 D  D  S  N  V  I  K  I  S  V  K  K  P  K  F  F  K  Y  Q  V  G  A  F  A  Y  M  Y  F  L  S  450

1370 CCAAAATCAGCCTGGTTCTACAGTTTTCAATCTCATCCCTTCACAGTCCTATCAGAAAGGCACAGAGATCCTAACAACCCAGATCAACTA 1459
 451 P  K  S  A  W  F  Y  S  F  Q  S  H  P  F  T  V  L  S  E  R  N  R  D  P  N  N  P  D  Q  L  480
```

FIG. 9B

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```
1460 ACTATGTACGTCAAAGCTAACAAGGGCATTACGAGAGTACTTCTTAGCAAAGTTCTAAGCGCTCCAAACCATACCGTTGATTGCAAGATT 1549
 481  T  M  Y  Y  K  A  N  K  G  I  T  R  V  L  L  S  K  Y  L  S  A  P  N  H  T  V  D  C  K  I   510
1550 TTCTTAGAGGGACCATATGGCGTAACTGTCCCTCACATTGCCAAACTTAAGAGAAATCTAGTAGGAGTAGCTGCGGGCCTCGGCGTGGCA 1639
 571  F  L  E  G  P  Y  G  V  T  V  P  H  I  A  K  L  K  R  N  L  V  G  V  A  A  G  L  G  V  A   570
1640 GCCATCTACCCCCATTTCGTAGAATGCCTTAGATTGCCTAGCACTGATCAACTGCAGCACAAGTTCTACTGGATCGTCAACGACCTTAGT 1729
 541  A  I  Y  P  H  F  V  E  C  L  R  L  P  S  T  D  Q  L  Q  H  K  F  Y  W  I  V  N  D  L  S   570
1730 CACCTTAAGTGGTTCGAAAACGAGCTACAATGGCTTAAGGAGAAATCTTGTGAAGTCTCTGTCATCTACACTGGGTCATCAGTGGAGGAT 1819
 571  H  L  K  W  F  E  N  E  L  Q  W  L  K  E  K  S  C  E  V  S  V  I  Y  T  G  S  S  V  E  D   600
1820 ACAAACTCAGATGAGTCCACTAAGGGTTTCGATGACAAGGAAGAATCTGAAATCACCGTAGAATGCCTTAACAAGAGGCCAGACCTCAAA 1909
 601  T  N  S  D  E  S  T  K  G  F  D  D  K  E  E  S  E  I  T  V  E  C  L  N  K  R  P  D  L  K   630
1910 GAGCTAGTGAGATCAGAGATCAAATTGTCAGAACTCGAGAACAACAACATCACTTTCTACTCATGCGGACCAGCGACTTTCAATGACGAC 1999
 631  E  L  V  R  S  E  I  K  L  S  E  L  E  N  N  N  I  T  F  Y  S  C  G  P  A  T  F  N  D  D   660
2000 TTTAGGAATGCAGTTGTACAAGGTATCGATTCTAGTCTGAAGATAGATGTCGAACTAGAGGAGGAGAGTTTTACTTGGTAA         2089
 661  F  R  N  A  V  V  Q  G  I  D  S  S  L  K  I  D  V  E  L  E  E  E  S  F  T  W  *         687
2090 ctt
```

FIG. 9C

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FRE1

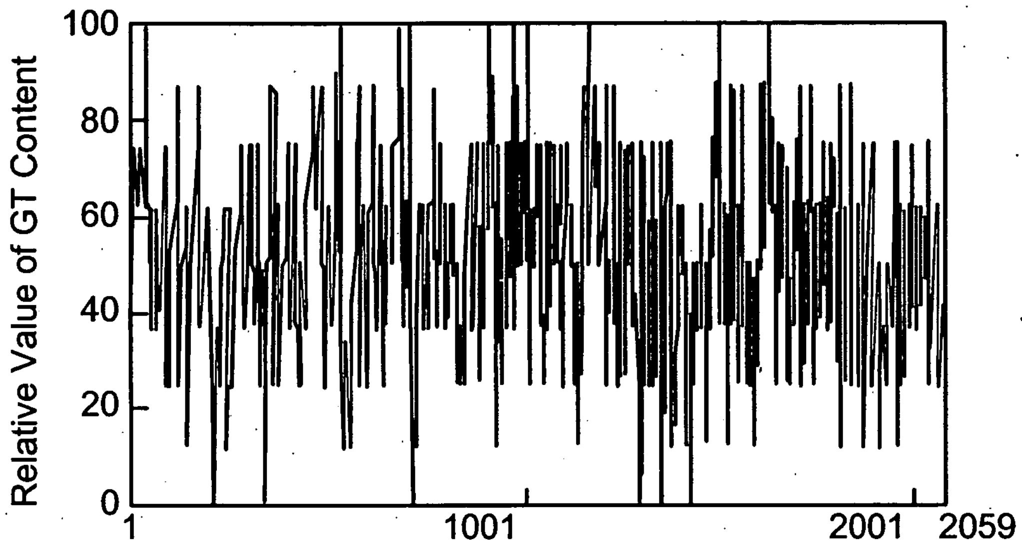

FIG. 10A

refre1

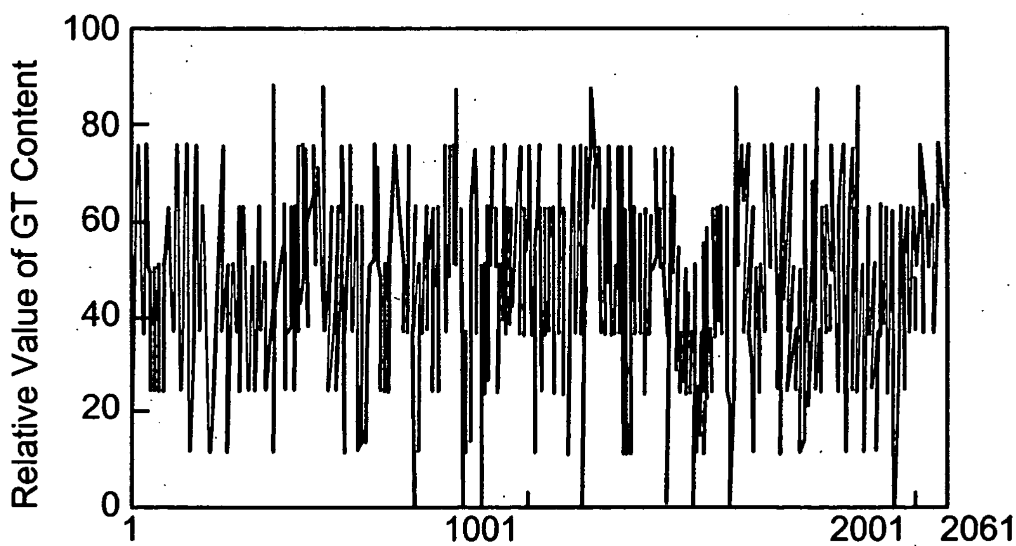

FIG. 10B

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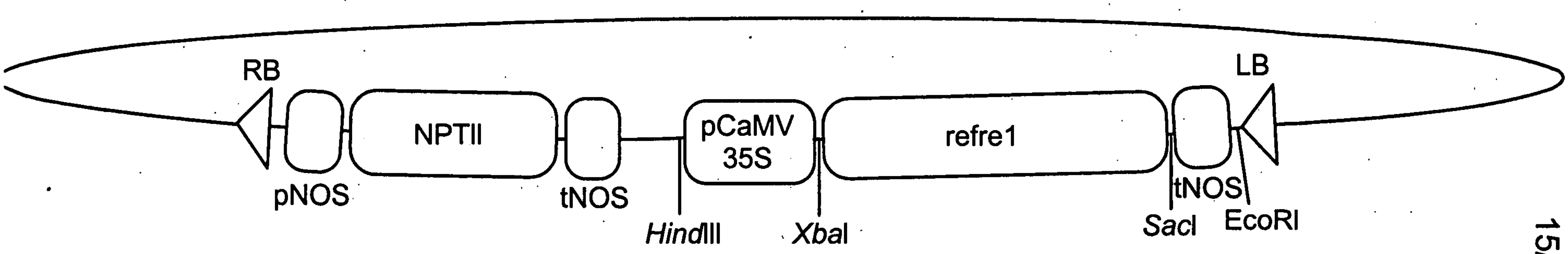

FIG. 11

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FIG. 13

FIG. 12

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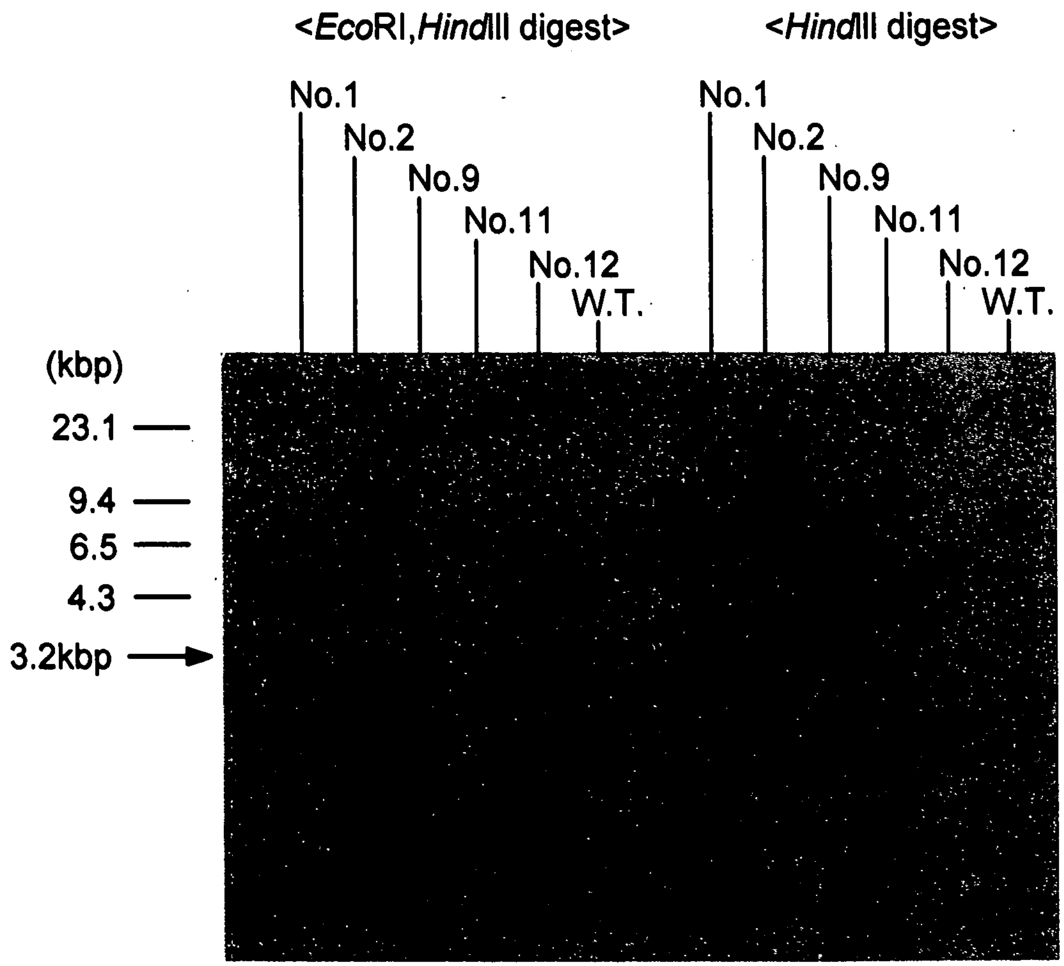

FIG. 14

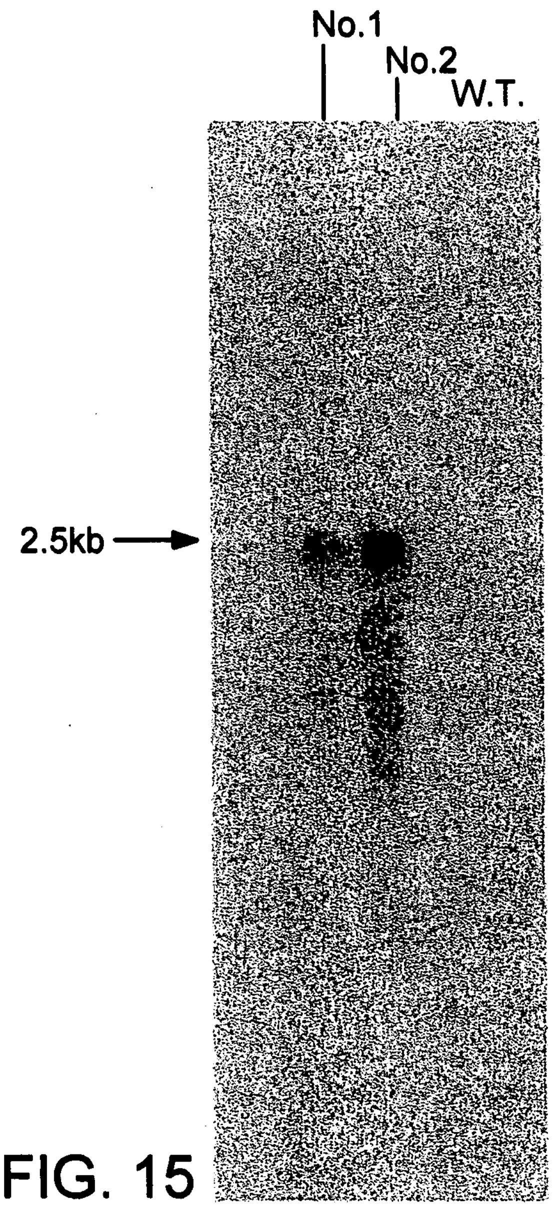

FIG. 15

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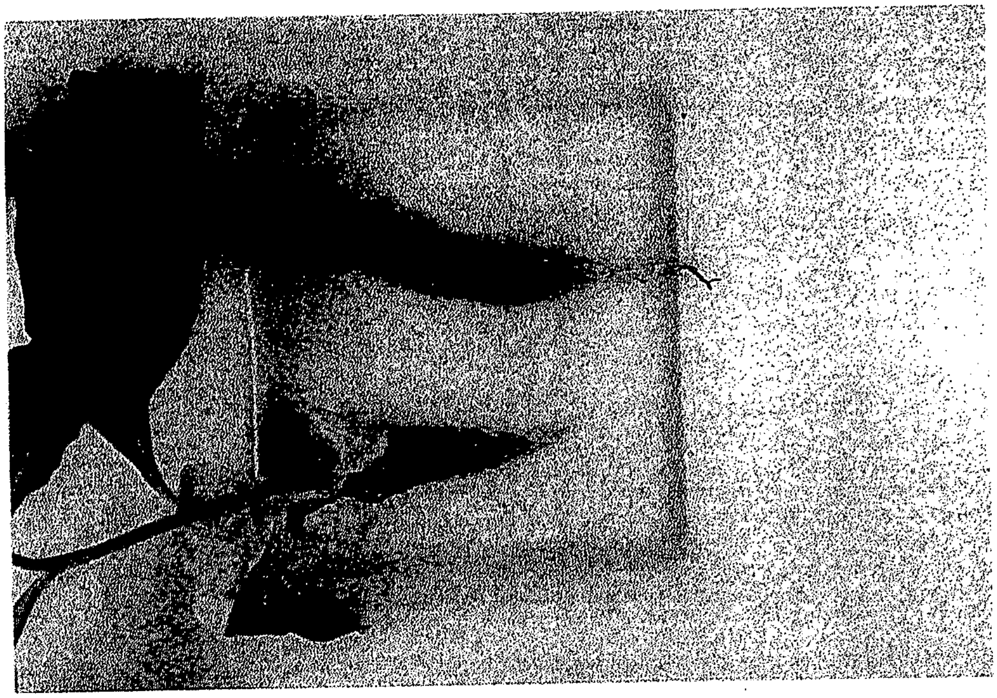

FIG. 17

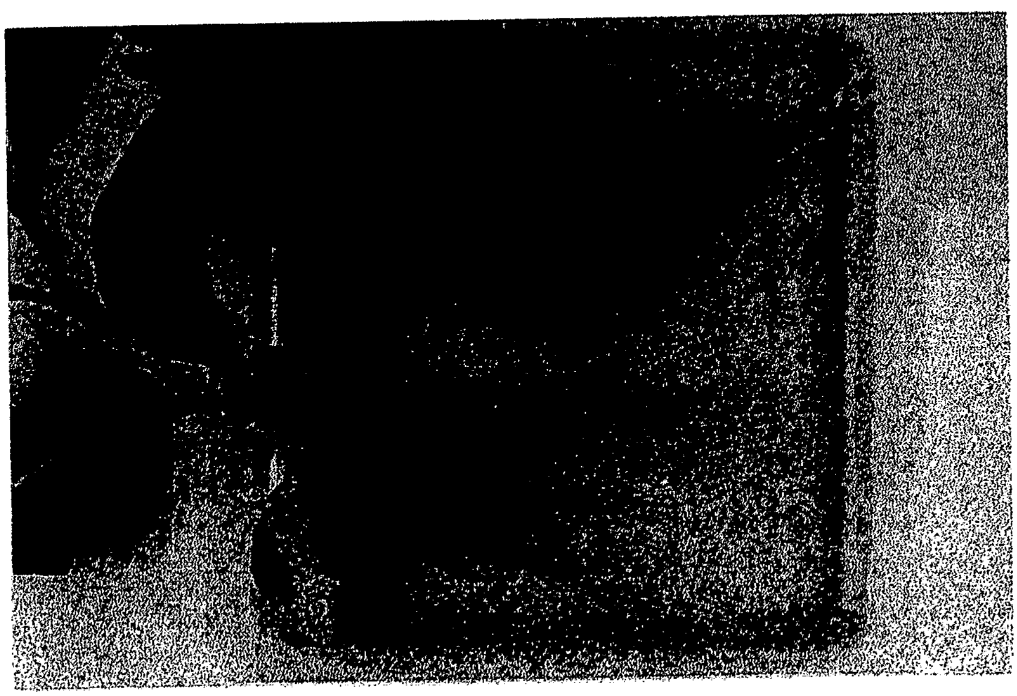

FIG. 16

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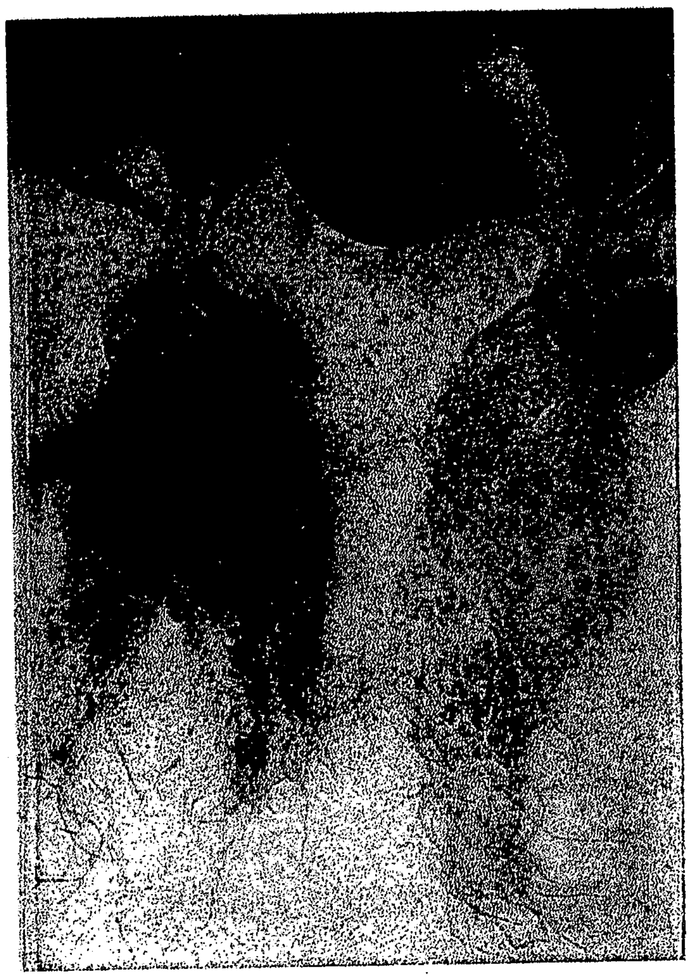

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FIG. 18